



Table IV: HLA Class I Standard Peptide Binding Affinity.

ALLEL	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	2109	25
A*0201	941.01	FLPSDYFPSV	2110	5.0
A*0202	941.01	FLPSDYFPSV	2111	4.3
A*0203	941.01	FLPSDYFPSV	2112	10
A*0205	941.01	FLPSDYFPSV	2113	4.3
A*0206	941.01	FLPSDYFPSV	2114	3.7
A*0207	941.01	FLPSDYFPSV	2115	23
A*6802	1072.34	YVIKVSARV	2116	8.0
A*0301	941.12	KVFPYALINK	2117	11
A*1101	940.06	AVDLYHFLK	2118	6.0
A*3101	941.12	KVFPYALINK	2119	18
A*3301	1083.02	STLPETYVVRR	2120	29
A*6801	941.12	KVFPYALINK	2121	8.0
A*2402	979.02	AYIDNYNKF	2122	12
B*0702	1075.23	APRTLVYLL	2123	5.5
B*3501	1021.05	FPFKYAAAF	2124	7.2
B51	1021.05	FPFKYAAAF	2125	5.5
B*5301	1021.05	FPFKYAAAF	2126	9.3
B*5401	1021.05	FPFKYAAAF	2127	10

↑
allele

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Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	SEQ ID	Sequence	Binding Affinity (nM)
DRB1*0101	DR1	515.01	2128	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	2129	YKTIAFDEEARR	300
DRB1*0401	DR4w4	515.01	2130	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	2131	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	2132	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	2133	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	2134	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	2135	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	2136	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	2137	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	2138	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	2139	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2 β 1	507.02	2140	GRTQDENPVVHFFK NIVTPRTPPP	9.1
DRB3*0101	DR52a	511	2141	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	2142	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2 β 2	553.01	2143	QYIKANSKFIGITE	20

bad clock

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table XIX
CEA DR₅ Super-Motif Peptides with

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w81	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12
IPNQVALLT	1962	RWCIPWORLITASL	7815	10	0.6100	0.0110	-0.0007	0.0150	0.0830		-0.0005	
WORLITASL	1963	CIPWORLITASL	7816	12								
I.LITASLTF	1964	WORLITASLTF	7817	15							-0.0022	
LITASLTF	1965	ORLLITASLTFWN	7818	16								
I.TASLTWN	1966	A.SLLITASLTFWNPP	7819	17								
LTWNPPTTKL	1967	ASLLITWNPPTTKL	7820	22								
FWNPPTTAK	1968	LLTEWNPPTTAKTL	7821	24								
WNPPTTAKL	1969	LTEWNPPTTAKTLIE	7822									
I.TESTPN	1970	TAKLITTESTPNIAF	7823	33								
LLVNPLPH	1971	EVLILLVNPLPHLFG	7824									
I.VNPIPOH	1972	VLLI.VNPIPOH.FGY	7825	51								
YGVEDVGN	1973	WSVKYKGERDVGDNRQI	7826	63								
IGYVGTCT	1974	NROQIVGVTGTOAT	7827	76								
IGTOATPG	1975	GVIYGTOATGTPAY	7828	81								
YSGRVYHP	1976	GPAYKGRVYHPYNS	7829	92								
IYPNSSL	1977	GREINYNPASNLL	7830	97							0.0029	
IYPNSSLJ	1978	REIYPNSSLJUNII	7831	98								
IYPNSSLIO	1979	EIYPNSSLJUNII	7832	99							-0.0005	
LLIONION	1980	ASLLIONIONQNDTG	7833	104								
LIONIOND	1981	ASLLIONIONQNDTG	7834									
IONDTCY	1982	IONIONQNDTGFTLH	7835	109								
FYTLLVIRKS	1983	DIGFYLLVIRKSDLV	7836	116								
YTHVKSID	1984	TGFYFTLHVKSID.VN	7837	117								
LHVKSIDLV	1985	FYTLLHVKSIDLVNEE	7838	119								
VKSDLVNEE	1986	TLHVKSIDLVNEEATG	7839	121								
IKSDELVNEE	1987	LHVKSIDLVNEEATG	7840	122							0.1300	
I.VNFATGOF	1988	KSDLNNEAEATGORY	7841	124							0.0058	
VNEATGOF	1989	SDLNNEAEATGORY	7842	126								
VPELPKPS	1990	ORFVYEPFLPKPSSS	7843	137								
LPKPSISSN	1991	YELPLPKPSISSNPKSS	7844	141							-0.0022	
ISNNPSKPV	1992	KPSISSNPSKPV	7845	145							-0.0022	
VEDKDAVF	1993	SKPVDEKDVAF	7846	154								
WNNNSNPV	1994	YLWWNNNSNPVSPR	7847	176								
WNNNSNPV	1995	LWWNNNSNPVSPR	7848	177								
I.TENVTRN	1996	NRTL.TENVTRNDA	7849	197								
LSCHASNP	1997	LFNVTNNTASYKE	7850	202								
VSARIDSY	1998	ONPVSAARRDSVIL	7851	218								
VILNVLYCP	1999	SDSVNLVLYCPDAP	7852	226								
I.YCPDAPTI	2000	I.NVL.YCPDAPTI	7853	231								
YCPDAPTI	2001	I.NVL.YCPDAPTI	7854	232								
ISPLINTSYR	2002	APLISPLINTSYR	7855									
I.TENVTRN	2003	NLSNLSCHAASNPFO	7856	254								
WPNNGTYC	2004	OYSWPNNGTYCOSTO	7857	268								
FLPNNTV	2005	TOELPNNTVTCOSTO	7858	281								
FINNTVNN	2006	OFLPNNTVNNNSG	7859	282								
IPNTVNNNS	2007	ELPNNTVNNNSG	7860	283								
ITVNNNSG	2008	IPNTVNNNSGTYCOAH	7861	286								
VNNNSGTYC	2009	NITYNNNSGTYCOAH	7862	288								
LNRTTVTTI	2010	DTGLNRTTVTTIYV	7863	305								
VTTTYYAE	2011	TRTTVTTIYVAPPK	7864	310								
YYAPPKPF	2012	TRTTVTTIYVAPPKPF	7865	315							0.0042	
ITSNNSPV	2013	KPTITSNNSPVDE	7866	324							-0.0022	
VEDAVAL	2014	SNPVEVEDAVALICE	7867	332							0.0054	
LTLTSVTRN	2015	NRLLTSLSTTRN	7868	375							-0.0022	
VTRNDVGPY	2016	LLSVTRNDVGPYEC	7869	380								
VCPYEGCIO	2017	RNDVGPYECGIOEL	7870	385								
IONELSVSDH	2018	ECGIONELSVSDH	7871	392								

SEQ ID No. 1

Column 1 to Column 4

Column 5 to Column 8



Table XIX
FA DB Super Motif Peptides with



Table XIX CEA DR Super Motif Peptides with Binding

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DRrw19	DR7	DRrw2	DR9	DRw33
IPWQRLLLT	1962	RWCIPWQRLLLTASL	1815	0.0110	0.0700	-0.0004		
WQLRLLT	1963	CIPWQRLLLTASL	1816					
LILTASLLT	1964	WQLRLLTASLTFW	1817					
LILTASLLTF	1965	QRLLI-TASLTFWNP	1818			-0.0013		
LTLASLLTF	1966	RLLLTASLTFWNPP	1819					
LTFWNPPT	1967	ASLLTFWNPPTAKL	1820					
FWNPPTA	1968	LTLTEWNPPTAKLTI	1821					
WNPPTAK	1969	LTFWNPPTAKLTI	1822					
LTIESTPEN	1970	TAKLTTESTPENYAE	1823					
LLVHLNPO	1971	EVLLVHLNPLQHFLG	1824					
LYHNLRPH	1972	VLLVHLNPLQHFLG	1825					
YKGERVQD	1973	YSWKGKGERVGDNRQ	1826					
IGGYVGTQ	1974	NRQIGGVYVGTQOAT	1827					
IGTQQATPG	1975	GYVIGTQQATPGAY	1828					
YSGREIYIP	1976	GPAYSGREIYIPNAS	1829					
IIPYNASLL	1977	GREIYPNASLLIQN	1830			0.0083		
IYPNASLLI	1978	REIYPNASLLIQN	1831					
YPNASLLIQ	1979	EIYPNASLLIQNII	1832			0.0029		
LLIQNQN	1980	NASLIQNIQNDTG	1833			-0.0013		
LQNIQND	1981	ASLIQNIQNDTG	1834					
IIQNQNDGFY	1982	IQNIIQNDGFYTLH	1835					
FYTLLHVIKSD	1983	DTGFYTLHVIKSDLV	1836					
YTLHVIKSD	1984	TOFTYTLHVIKSDLVN	1837					
LHVIKSDLV	1985	FYTLLHVIKSDLVN	1838					
VIKSDLVNE	1986	TLHVIKSDLVNNEAT	1839					
IKSDLVNEE	1987	LHVIKSDLVNEAT	1840					
LVNEEATG	1988	TKSDLVNEEATGQFRRV	1841					
VNEEATGQ	1989	SDLVNEEATGQFRVV	1842					
VPELPKRP	1990	QFRVPELPKRPSSS	1843					
LPKPSISSN	1991	YPLPKPSISSNNSK	1844			-0.0013		
ISSNNNSKPV	1992	KPSISSNNNSKPVDEK	1845			0.0033		
VEDKDAVA	1993	SKPVEDKDAVAFTCE	1846					
WYNQNSLP	1994	YLWWYNNQSLPVSP	1847					
VNNQSLPV	1995	LWWYNNQSLPVSPR	1848					
LTLFVNTR	1996	NRTLTLFVNTRNTDA	1849					
VTRNTDAS	1997	LFNTRTRNDTASYKCE	1850					
VSARSDS	1998	ONPVSAARRSDSVILN	1851					
VILNLVGP	1999	SDSVILNLVYGPDAP	1852					
LYGPDAPI	2000	LNLVYGPDAPIISPL	1853					
YGPDAPI	2001	NVLVYGPDAPIISPL	1854					
ISPLNTSYR	2002	APTSPLNTSYRSGE	1855					
LSCHAASN	2003	NLNLSCHAASNPAQ	1856					
WFVNGTFO	2004	QTSWFVNGTFOQST	1857					
LEPNITVNN	2005	TOELPNITVNNNG	1858					
FIPNTVNN	2006	QELFIPNTVNNSGS	1859					
IPNTVNN	2007	ELFIPNTVNNSGSY	1860					

more known

first or others



CEA DR Super Motif Peptides with Binding



Table XIX CEA DR Super Motif Peptides with Binding

Core Sequence	Exemplary SeqID Num	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FVSNLATG	2054	YACFVSNLATGRNN	1907	0.0070			
VSNLATGR	2055	ACFVSNLATGRNN	1908				
IVKSIIVSA	2056	NNISIVKSIIVSAGT	1909	0.0690	0.0370	0.0120	
YKSITVSA	2057	NSIVKSIIVSAGT	1910	0.0460	0.0760	0.0170	
YKSITVSA	2058	VKSITVSAGSTSPGL	1911				
ITVSAGTS		SITVSAGTSAGTSPGLA					
VSAGTSP	2059	SPGLSAGATGVIMIG	1912				
LSAGATVG	2060	TVGIMIGVLVGVALI	1913				
IMGVLVGV	2061	TAKLTIESTPNVAE	1914				
LTIESTPFN	2062	YSWYKGGERVDGNRO	1915				
YKGERTDG	2063	NOSLPLSPRLQSLNG	1916				
LPVSPLRQ	2064	GENLNLSCHAASNPP	1917				
LNLSCHA	2065	GQSLPVSPRLQSLNG	1918				
LPVSPLRQ	2066		1919				

(SEE TD 100%)

Wrote Searched
all done



Seq ID No:

Table XXa
CEA DR 3a Motif Peptides with Binding
Exemplary Position SeqID Num.

Core Sequence	Core SeqID Num.	Exemplary Sequence	Exemplary Position	SeqID Num.
IQNDTGFYT	2067	QNIQNDTGFYTLLHV	1920	110
IKSDLVNE	2068	LHVLISDLVNEATGQF	1921	122
LVNEEATGQ	2069	KSDLVNEEATGQFRV	1922	126
VNEEATGQF	2070	SDLVNEEATGQFRVY	1923	127
VYPELPKPS	2071	QFRVYPELPKPSISS	1924	137
FTCEPEIQD	2072	A V A F T C E P E I Q D A T Y	1925	-
YRCETQNPV	2073	T A S Y K C E T O N Q P V S A R	1926	210
YGPDAPIIS	2074	N V L Y G P D A P I T S P L N	1927	232
VYALEPKPF	2075	T I T V Y A E P K P F T S	1928	315
VEDEDAVAL	2076	S N P V E D E D A V A L T C E	1929	332
LTCPEFIQN	2077	A V A L T C E P E I Q N T Y	1930	340
IQNELSVQH	2078	E C Q I N E L S V H D S D P	1931	392
LSVDHSDPV	2079	Q N E L S V D H S D P V I L N	1932	396
YGPDDPITS	2080	N V L Y G P D D P I T S P Y	1933	410
VSAELPKPS	2081	T I T V S A E L P K P S I S S	1934	493
FTCEPEAQN	2082	A V A F T C E P E A Q N T Y	1935	-
VTLDVLYGP	2083	S D P V T L D V L Y G P D T P	1936	518
YGPDTIPS	2084	D V L Y G P D T P I S P P D	1937	582
				588
				0.00037
				-0.0008

*in use 0 8000
last 6 days*

ordered



Table XXa CEA DR 3a Motif Peptides with Binding Data

Core Sequence	Exemplary SeqID Num	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
IQNDTGFYT	2067	QNIQNDTGFYTILHV					
IKSDLVNEEATG	2068	LHVIKSDLVNEEATG	1920	0.3600	-0.0017	-0.0009	
LYNNEATGQ	2069	KSDLVNEEATGQFRV	1921				
VNEATGQF	2070	SDLVNEEATGQFRV	1922				
VYELPKPS	2071	QFRVYELPKPSISS	1923				
FTCEPETOQD	2072	A VAFITCEPETOQD	1924				
YKCETONPV	2073	TASVTKCETONPV	1925				
YGPDAPTIS	2074	TSVTKCETONPV SAR	1926				
VIAEPPKPF	2075	NVL YGPDAPTISPLN	1927				
VIEDVEDAVAL	2076	TITVVAEPPKPFITS	1928				
LTCPEEQN	2077	SNPVEDEDAVALTCE	1929				
IQNELSDVH	2078	AVALTCEPEQNTTY	1930				
LSVDHSDPV	2079	ECCIONELSYDHSDP	1931				
YGRDDTPIS	2080	QNELSVDHSDPVILN	1932				
VSAELPKPS	2081	NVL YGPDDDTISPY	1933				
FTCEPEAQN	2082	TITVSAELPKPSISS	1934				
VTLDVLYGP	2083	A VAFITCEPEAQNTTY	1935				
YGRDTTIPS	2084	SDPVTLVDVLYGPDT	1936				
		DVLYGPDTTIPSPPD	1937				

last
of series
of three in

CEA DR 3a



Table XXb

CEA DR 3b Motif Peptides with Binding Data

Core Sequence	Core Seq ID Num	Exemplary Sequence	Exemplary Seq ID Num	Position	DR1	DR2w181	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12
ATGFRVYP	2085	NEEATQFRVYPPELP		131							-0.0027	
LNTSYRSGE	2086	ISPLNTSYRSGENLW	1939	242							-0.0027	
YTCQAHNSD	2087	SGSYTCAHNSDTGL	1940	294							-0.0027	
LPVSPLRLQL	2088	NQSLPVSPRLQLSND	1941	360							0.0071	
LSNDNRTLT	2089	RLOLSNDNRTLTLLS	1942	368	0.0001	-0.0006	-0.0007				-0.0055	0.0008
LSSLCHSAS	2090	GVLNLSSCHASASNPP	1943	430							0.0075	
LNLCHSAS	2091	GANLNLSCHASANPS	1944	608							-0.0027	
ASPERTHLM	2092	RLPASPERTHLDMLRH	1945	34							-0.0027	
AHNQYRQVP	2093	VLAHNQYRQVPLQR	1946	84							0.0290	
LDTTDRSRACH	2094	ALTLCDTDRSRACHP	1947	180							0.0150	
IHHHTHLCFVHT	2095	LAUHHHTHLCFVHT	1948	465	0.0140	0.0590	0.0009				-0.0055	0.0025
LFRPHQAL	2096	WDQFLRPHQALLLHT	1949	482	-0.0001	0.0615	-0.0007				0.9000	-0.0055
VDLDKGCP	2097	HSCVLDLDKGCPAEQ	1950	632							-0.0027	
YLEDYRLVH	2098	GMSTYLEDYRLVHVRDL	1951	832							0.1800	
IDSECBRFE	2099	CWMIDSECBRFE	1952	958	0.0036	-0.0306	0.0150				-0.0008	
AAQPQHPPP	2100	QGGAAQPQHPPPFFS	1953	120							-0.0023	
AAISRKAWE	2101	EFGQAISRKAWEVLYH	1954	104							0.0039	
LHHTLKIGG	2102	VKLHLHTLKIGGEPH	1955	284							-0.0025	
IGGEPHISTPPL	2103	TLKIGGEPHISTPPL	1956	290							-0.0025	
AAISRKAWE	2104	EFGQAISRKAWEVLYH	1957	104							0.0027	
ILGPDKKL	2105	EDSILGPDKKLTH	1958	235	0.0003	-0.0006	-0.0010				-0.0035	
YKSOHIMTE	2106	MALKQSQMHTEVVR	1959	160							-0.0025	
VEGNLRVEY	2107	LIRVEGNRVEYLLD	1960	194							0.0930	
FTLQICRCRE	2108	GEYFTLQICRCRE	1961	325							0.0290	

more from last column

Table XXb
CEA DR3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9
ATGQFRVYP	2085	NEATIGQFRVYPPELP	1938				
LNTSYRSGE	2086	ISPLNTSYRSGEINLN	1939				
YTCOHNSD	2087	SCSYTCOAHNSDITGL	1940				
LFPSRQLQ	2088	NOSLPYSPLQLQSNL	1941				
LSNDNRLTLL	2089	RQLSNDRNLRTLLS	1942				
LSLCHAS	2090	GYNLSLSCHASNPP	1943				
LNL SCHSAS	2091	GANLNSCHSASNSPNS	1944				
ASPETHLD	2092	RLPASPETHLDMLRH	1945				
AHQYRQVP	2093	VLAHNQYRQVPQQR	1946				
LDTNRRA	2094	ALTLDTNRRAACHP	1947				
IHHNTHLCF	2095	LALIHNTHLCFVHT	1948	0.0200	0.0200	0.0330	
LPRNPHQAL	2096	WDOLERNPHQALHT	1949	0.0410	-0.0017	-0.0009	
VDLDDKGCP	2097	HCFVLDLDKGPQ	1950				
YLEDVRLVH	2098	GRSAYLEDVRLVHDL	1951				
IDSCRERF	2099	CWMDISCREPRFREL	1952	(0.0001)	-0.0014	0.0028	
APOPQHPP	2100	QGGAAPQHPPAFS	1953				
AASRKAVAE	2101	EFOQAISRKAVAEVH	1954				
LHHTLKKG	2102	VAVLHTLKKGEGPH	1955				
ICGPHISY	2103	TLKIGGPHISYPP	1956				
AASRKVAE	2104	EFOQAASRKVAELVH	1957				
ILGPBKLL	2105	EDSILGDPKKLTOH	1958				
YKQSORMITE	2106	MAYKQSORMITEYVR	1959				
VEGNLRVEY	2107	LIRVEGNLRVEYLD	1960				
FTLQRCRE	2108	GEYFTLQRCRE	1961				

more down
less down

O I P E
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Table XXII. Cr ss-reactive binding of CEA analog peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Bound
CEA.24	9	LLTFWNPPPT	2144	179	1720	67	755	-- ²	2
CEA.24M2V9	9	LMTFWNPVV	2145	4.5	782	7.7	34	3333	3
CEA.24V9	9	LLTFWNPPV	2146	16	307	26	56	952	4
CEA.78	9	QIIGYVIGT	2147	313	148	106	100	150	5
CEA.78L2V9	9	QLIGYVIVGV	2158	9.4	5.9	2.3	21	2.3	5
CEA.233	10	VLYGPDAPTI	2149	128	606	270	804	--	2
CEA.233V10	10	VLYGPDAPTV	2150	26	430	16	206	952	4
CEA.411	10	VLYGPDDPTI	2151	294	358	476	7400	--	3
CEA.411V10	10	VLYGPDDPTV	2152	161	105	91	2467	--	3
CEA.569	9	YVCGIQNSV	2153	98	358	159	80	181	5
CEA.569L2	9	YLCGIQNSV	2154	50	24	12	31	3478	4
CEA.589	9	VLYGPDTPI	2155	200	878	53	638	--	2
CEA.589V9	9	VLYGPDTPV	2156	20	165	91	154	9756	4
CEA.605	9	YLSGANLNL	2157	28	165	2.4	804	--	3
CEA.605V9	9	YLSGANLNV	2158	73	13	13	80	1600	4
CEA.687	9	ATVGIMIGV	2159	36	8.8	20	11	0.80	5
CEA.687L2	9	ALVGIMIGV	2160	10	63	31	100	102	5
CEA.691	9	IMIGVLVGV	2161	69	62	13	106	89	5
CEA.691L2	9	ILIGVLVGV	2162	22	8.0	3.2	16	160	5

1) Wild-type peptides presented for reference purposes.

2) -- indicates binding affinity =10,000nM.

add



TABLE XXII A A01 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*0101 nM</u>
52.0105	11	RVDGNRQIIGY	2163	CEA.72	294.1
52.0109	11	RSDSVILNVLY	2164	CEA.225	47.2
52.0113	11	HSDPVILNVLY	2165	CEA.403	25.8
52.0116	11	RSDPVTLDVLY	2166	CEA.581	7.8
57.0004	9	QQDTPGPAY	2167	CEA.87.D3	56.8
57.0007	9	AADNPPAQY	2168	CEA.261.D3	45.5
57.0008	9	ITDNNNSGSY	2169	CEA.289.D3	96.2
57.001	9	VTDNDVGPY	2170	CEA.383.D3	4.1
57.0011	9	PTDSPSYTY	2171	CEA.418.D3	37.9
57.0012	9	TIDPSYTYY	2172	CEA.419.D3	3.1
57.0013	9	AADNPPAQY	2173	CEA.439.D3	44.6
57.0014	9	ITDKNSGLY	2174	CEA.467.D3	11.9
57.0103	10	PTDSPLNTSY	2175	CEA.240.D3	266
57.0104	10	PTDSPSYTYY	2176	CEA.418.D3	1.1
57.0105	10	HTASNPSPQY	2177	CEA.616.T2	131.6
57.0106	10	HSDSNPSPQY	2178	CEA.616.D3	44.6

add dock



Table XII B A03 Analog Peptides

Peptide	AA	SEQ ID NO:	Source	$\Delta^{*}0301 \text{ nM}$	$\Delta^{*}1101 \text{ nM}$	$\Delta^{*}3101 \text{ nM}$	$\Delta^{*}3301 \text{ nM}$	$\Delta^{*}6801 \text{ nM}$	$\Delta^{*}XRN$
1371.01	10	TVSPPLNTSYR	2179	CEA.241.V2	458.3	54.5	187.5	557.7	8.7
1371.02	10	TVSPPLNTSYK	2180	CEA.241.V2K10	16.9	6.3	10588.2	-48333.3	7.3
1371.03	10	RVLTLLSVTR	2181	CEA.376.V2	343.8	222.2	11.3	6041.7	666.7
1371.04	10	RVLTLLSVTK	2182	CEA.376.V2K10	37.9	50	163.6	-72500	5714.3
1371.05	10	TVSPSYTYR	2183	CEA.419.V2	2340.4	3000	29	263.6	8.6
1371.06	10	TVSPSYTYK	2184	CEA.419.V2K10	68.8	42.9	3673.5	26363.6	6.7
1371.07	9	IVPSYTYR	2185	CEA.420.V2	91.7	13.3	25.7	58	2.6
1371.08	9	IVPSYTYK	2186	CEA.420.V2K9	17.2	54.5	720	4328.4	21.6
1371.09	10	RVLTLFNVTR	2187	CEA.554.V2	297.3	93.8	9	7631.6	42.1
1371.1	10	RVLTLFNVTK	2188	CEA.554.V42K10	20.8	31.6	233.8	41428.6	2352.9
1371.13	9	FVSNLATGK	2189	CEA.656.K9	1466.7	206.9	-36000	-72500	5.3



Table XXIIC A24 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO.	Source	A*2401 nM
52.0033	8	IYPNASLL	2190	CEA.101	176.5
52.0038	8	SWFVNNGTF	2191	CEA.270	480
52.0137	11	RWCIPWQRLLL	2192	CEA.10	151.9
52.0138	11	PWQRLLTASL	2193	CEA.14	324.3
52.0141	11	FYTLHVIKSDL	2194	CEA.119	480
52.0142	11	TYLWWVNNQSL	2195	CEA.175	85.7
52.0144	11	TYLWWVNNQSL	2196	CEA.353	46.2
52.0145	11	SYTYYRPGVNL	2197	CEA.423	218.2
52.0146	11	TYYRPGVNLSL	2198	CEA.425	131.9
52.0147	11	TYLWWVNGQSL	2199	CEA.531	92.3
57.0036	9	RYCIPWQRF	2200	CEA.10.Y2F9	190.5
57.0037	9	IYPNASLLF	2201	CEA.101.F9	2.2
57.0038	9	LYWVNQNQSF	2202	CEA.177.Y2F9	63.2
57.0039	9	LYGPDAPTF	2203	CEA.234.F9	63.2
57.0041	9	TYYRPGVNF	2204	CEA.425.F9	52.2
57.0042	9	LYWVNQGSF	2205	CEA.533.Y2F9	15.8
57.0044	9	QYSWRINGF	2206	CEA.624.F9	109.1
57.0045	9	TYACFVSNF	2207	CEA.652.F9	8.6
57.0072	10	RYCIPWQRLF	2208	CEA.10.Y2F10	26.1
57.0073	10	FYNPPTTAKF	2209	CEA.27.Y2F10	181.8
57.0074	10	VYPELPKPSF	2210	CEA.140.F10	106.2
57.0075	10	TYQQSTQELF	2211	CEA.276.Y2	307.7
57.0076	10	VYAEPPPKPFF	2212	CEA.318.F10	26.7
57.0077	10	YYRPGVNLSF	2213	CEA.426.F10	10
57.0078	10	QYSWLDGNF	2214	CEA.446.F10	60
57.0079	10	SYLSGANLNF	2215	CEA.604.F10	10

↓
add add



Table XXXIII. Immunogenicity of A2 supermotif-bearing peptides

Peptide	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*6802 nM	No. A2 Alleles Bound	CTL Peptide ¹	CTL Wild-type	CTL Tumor
CEA.78	9	QLGYVIGT	2216	313	148	106	100	151	5	0/3	
CEA.354	10	YLWWVNQSL	2217	26	108	26	487	333	5	1/2	0/1
CEA.569	9	YVCGIQNSV	2218	98	358	159	80	182	5	1/2	0/1
CEA.605	9	YLSGANLNL	2219	28	165	2	804	-- ²	3	2/2	1/2
CEA.687	9	ATVGIMIGV	2220	36	9	20	11	1	5	1/1	1/1
CEA.691	9	IMIGVLVGV	2221	69	62	13	106	89	5	8/8	4/7
CEA.24	9	LLTFWNPPT	2222	179	1720	67	755	-- ²	2	0/1	0/1
CEA.24V9	9	LLTFWNPPV	2223	16	307	26	56	952	4	1/1	1/1
CEA.233	10	VLYGPDAPTI	2224	128	606	270	804	--	2	2/4	0/3
CEA.233V10	10	VLYGPDAPTV	2225	26	430	16	206	952	4	3/4	2/2
CEA.589	9	VLYGPDPTI	2226	200	878	53	638	--	2	1/1	0/1
CEA.589V9	9	VLYGPDPTPV	2227	20	165	91	154	9756	4	2/2	0/2
CEA.605	9	YLSGANLNL	2228	28	165	24	804	--	3	2/2	1/2
CEA.605V9	9	YLSGANLNV	2229	73	13	13	80	1600	4	4/4	3/4

1) Number of donors yielding a positive response/total tested.

2) - indicates binding affinity = 10,000nM.

add add

Table XXXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide		SEQ ID NO:
				Source	Sequence	
Human	A1	A*0101	Steinlin	Hu J chain	YTAVVPLVY	2230
	A2	A*0201	JY	HBVC 18-27 F6->Y	FLPSDYFPSV	2231
	A2	A*0202	P815 (transfected)	HBVC 18-27 F6->Y	FLPSDYFPSV	2232
	A2	A*0203	FUN	HBVC 18-27 F6->Y	FLPSDYFPSV	2233
	A2	A*0206	CLA	HBVC 18-27 F6->Y	FLPSDYFPSV	2234
	A2	A*0207	721.221 (transfected)	HBVC 18-27 F6->Y	FLPSDYFPSV	2235
	A3	GM3107		non-natural (A3'CON1)	KVFPYALINK	2236
	A11	BVR		non-natural (A3'CON1)	KVFPYALINK	2237
	A24	A*2402	KAS116	non-natural (A24'CON1)	AYIDNYNKF	2238
	A31	A*3101	SPACH	non-natural (A3'CON1)	KVFPYALINK	2239
	A33	A*3301	LWAGS	non-natural (A3'CON1)	KVFPYALINK	2240
	A28/68	A*6801	C1R	HBVC 141-151 T7->Y	STLPETTYVRR	2241
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL	2242
	B7	B*0702	GM3107	A2 signal seq. 5-13 (L7->Y)	APRTLVYLL	2243
	B8	B*0801	Steinlin	HIV gp 386-593 Y1->F, Q5->Y	FLKPYQLL	2244
	B27	B*2705	LG2	R 60s	FRYNGLIRH	2245
	B35	B*3501	C1R, BVR	non-natural (B35'CON2)	PPFKYAAAF	2246
	B35	B*3502	TISI	non-natural (B35'CON2)	PPFKYAAAF	2247
	B35	B*3503	EHM	non-natural (B35'CON2)	PPFKYAAAF	2248
	B44	B*4403	PITOUT	EF-1 G6->Y	ADMGRYSFY	2249
	B51	B*5301	KAS116	non-natural (B35'CON2)	PPFKYAAAF	2250
	B53	B*5401	AMAI	non-natural (B35'CON2)	PPFKYAAAF	2251
	B54	Cw*0401	KT3	non-natural (B35'CON2)	PPFKYAAAF	2242
	Cw4	Cw*0602	C1R	non-natural (C4'CON1)	QYDDAVYKL	2243
	Cw6	Cw*0702	721.221 transfected	non-natural (C6'CON1)	YRHDDGNVL	2254
	Cw7	Cw*0702	721.221 transfected	non-natural (C6'CON1)	YRHDDGNVL	2255
Mouse	D ^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI	2256
	K ^b		EL4	VSV NP 52-59	RGYVFQQL	2257
	D ^d		P815	HIV-IIIB ENV G4->Y	RGPYRAFVTI	2258
	K ^d		P815	non-natural (KdCON1)	KFNPDMKTYI	2259
	L ^d		P815	HBVs 28-39	IPQSLSDYWTSL	2260





B. Class II binding assays

Species	Antigen	Allele	Cell line	Source	Sequence	Radio-labeled peptide	SEQ ID NO.
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKVKQNTLKLAT	VVHFFKNIVTRTPPY	2261
	DR2	DRB1*1501	L466.1	M6P 88-102Y	YAAFAAKATAAAFA	YAAFAAKATAAAFA	2262
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YKTIAFDEEARR	YKTIAFDEEARR	2263
	DR3	DRB1*0301	MAT	MT 65KD Y3-13	YARFQSQTTLKQKT	YARFQSQTTLKQKT	2264
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQRQTTLKAAA	YARFQRQTTLKAAA	2265
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQSQTTLKQKT	YARFQSQTTLKQKT	2266
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT	YARFQSQTTLKQKT	2267
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	QYIKANSKFIGITE	QYIKANSKFIGITE	2268
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE	QYIKANSKFIGITE	2269
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE	QYIKANSKFIGITE	2270
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE	QYIKANSKFIGITE	2271
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE	QYIKANSKFIGITE	2272
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	EALIHQLKINPVLS	EALIHQLKINPVLS	2273
	DR12	DRB1*1201	Herluf	unknown eluted peptide	QYIKANAKFIGITE	QYIKANAKFIGITE	2274
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE	QYIKANAKFIGITE	2275
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	PKYVKQNTLKLAT	PKYVKQNTLKLAT	2276
	DR51	DRB5*0201	L255.1	HA 307-319	NGQIQNDPNRDIL	NGQIQNDPNRDIL	2277
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	YARFQSQTTLKQKT	YARFQSQTTLKQKT	2278
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YAHAAHAAHAAHAAHAA	YAHAAHAAHAAHAAHAA	2279
	DQ3.1	QA1*0301/DQB1*0301	PF	non-natural (ROIY)	YAHAAHAAHAAHAAHAA	YAHAAHAAHAAHAAHAA	2280
Mouse	IA ^b		DB27.4	non-natural (ROIY)	YAHAAHAAHAAHAAHAA	YAHAAHAAHAAHAAHAA	2281
	IA ^c		A20	non-natural (ROIY)	YAHAAHAAHAAHAAHAA	YAHAAHAAHAAHAAHAA	2282
	IA ^c		CH12	HEL 46-61	YNTDGSTDYGILQINSR	YNTDGSTDYGILQINSR	2283
	IA ^c		LS102.9	non-natural (ROIY)	YAHAAHAAHAAHAAHAA	YAHAAHAAHAAHAAHAA	2284
	IA ^c		91.7	non-natural (ROIY)	YAHAAHAAHAAHAAHAA	YAHAAHAAHAAHAAHAA	2285
	IE ^d		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK	YLEDARRKKAIYEKKK	2286
	IE ^e		CH12	Lambda repressor 12-26	YLEDARRKKAIYEKKK	YLEDARRKKAIYEKKK	2287

add add



Table XXVI. Crossbinding data of A2 supermotif peptides.

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
CEA.24	9	LLTFWNNPPT	2288	179	1720	67	755	--	2
CEA.78	9	QIIGYVIGT	2289	313	148	106	100	150	5
CEA.233	10	VLYGPDPPTI	2290	128	606	270	804	--	2
CEA.354	10	YLWVVNNQSL	2291	26	108	26	487	67	5
CEA.411	10	VLYGPDDPTI	2292	294	358	476	7400	--	3
CEA.432	9	NLSLSCHAA	2293	455	2867	1449	18500	--	1
CEA.532	10	YLWWVNGQSL	2294	33	331	21	2056	286	4
CEA.569	9	YYCGIQNSV	2295	98	358	159	80	181	5
CEA.589	9	VLYGPDPPTI	2296	200	878	53	638	--	2
CEA.605	9	YLSGANLNL	2297	28	165	2.4	804	--	3
CEA.687	9	ATYGIMIGV	2298	36	8.8	20	11	0.80	5
CEA.690	10	GIMIGVLGVV	2299	64	205	31	142	500	5
CEA.691	9	IMIGVLGVV	2300	69	62	13	106	89	5
CEA.691	10	IMIGVLGVVA	2301	227	68	44	726	1509	3

-- indicates binding affinity = 10,000nM.

added



Table XXVII. Immunogenicity of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles	CTL	CTL
									Crossbound	Wild-type	Tumor
CEA.78	9	QIIGYVIGT	2302	313	148	106	100	151	5	0/3	
CEA.354	10	YLWWVNQSL	2303	26	108	26	487	333	5	1/2	0/1
CEA.569	9	YVCGIQNSV	2304	98	358	159	80	182	5	1/2	0/1
CEA.605	9	YLSGANLNL	2305	28	165	2.4	804	-- ²	3	2/2	1/2
CEA.687	9	ATYGIMIGV	2306	36	8.8	20	11	0.80	5	1/1	
CEA.691	9	IMIGVLVGV	2307	69	62	13	106	89	5	8/8	4/7

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

a. b. c. d. e.



Table XXVIII. Immunogenicity A2 supermotif analog peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Crossbound Alleles	CTL Peptide 1	CTL Wild-type	CTL Tumor
CEA:24	9	LLTFWNPPPT	2308	179	1720	67	755	-- ²	2	0/1	0/1	0/1
CEA:24V9	9	LLTFWNPPV	2309	16	307	26	56	952	4	1/1	1/1	1/1
CEA:233	10	VLYGDDAPTI	2310	128	606	270	804	--	2	2/4	2/4	0/3
CEA:233V10	10	VLYGDDAPTV	2311	26	430	16	206	952	4	3/4	2/2	1/4
CEA:389	9	VLYGDDTP1	2312	200	878	53	638	--	2	1/1	0/1	0/1
CEA:389V9	9	VLYGDDTPV	2313	20	165	91	154	9756	4	2/2	2/2	0/2
CEA:605	9	YLSGANLN	2314	28	165	24	804	--	3	2/2	2/2	1/2
CEA:605V9	9	YLSGANLNV	2315	73	13	13	80	1600	4	4/4	3/4	1/4

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.



Table XXIX. DR supertype primary binding

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- reactivity
39.0217	2	RWCIPWQRLLLTLASL	2316	CEA.10	8.2	542	357	3
39.0218	3	QRLLLTASLLTFWNP	2317	CEA.16	--	--	--	0
39.0219	2	EVLLLVLHNLQPQHLFG	2318	CEA.50	2.0	52	53	3
39.0220	3	GREIIYPNASLLIQN	2319	CEA.97	8.1	484	45	3
39.0221	2	EIIYPNASLLIQNII	2320	CEA.99	14	1154	156	2
39.0222	2	NASLLIQNIIQNDTG	2321	CEA.104	4546	--	--	0
39.0223	3	DTGFYTLHVIKSDLV	2322	CEA.116	69	1731	227	2
39.0224	2	YPELPKPSISSLNSK	2323	CEA.141	5556	--	--	0
39.0225	2	KPSISSNNSKPVEDK	2324	CEA.146	2381	--	7576	0
39.0226	3	YLWWVNNQSLPVSPR	2325	CEA.176	0.59	8.0	42	3
39.0227	3	LWWVNNQSLPVSPRL	2326	CEA.177	217	1552	3049	1
39.0228	2	QYSWFVNCTFQQSTQ	2327	CEA.268	192	80	926	3
39.0229	2	DTGLNRRTVTITVY	2328	CEA.305	--	--	2841	0
39.0230	2	KPFITSNSNPVEDE	2329	CEA.324	--	--	--	0
39.0231	2	NRTLTLSSVTRNDVG	2330	CEA.375	238	--	--	1
39.0232	2	QELFISNITEKNSGL	2331	CEA.460	--	2500	--	0
39.0233	3	RTTVKTITVSAELPK	2332	CEA.488	455	7031	317	2
39.0234	2	SAELPKPSISSLNSK	2333	CEA.497	--	--	--	0
39.0235	2	LDVLYGPDTPPISSPP	2334	CEA.587	--	--	--	0
39.0236	2	TQVLFIAKITPNNNG	2335	CEA.637	61	--	6579	1
39.0237	2	QVLFIAKITPNNNGT	2336	CEA.638	42	1875	--	1
39.0238	3	YACFVSNLATGRNNS	2337	CEA.653	208	1667	3571	1
39.0239	2	NNIVKSITVSASGT	2338	CEA.665	91	25	676	3
39.0240	3	NSIVKSITVSASGTS	2339	CEA.666	78	25	329	3

-- indicates binding affinity = 10,000nM.

↓
added



Table XXX DR supertype crossbinding

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2β1 nM	DR2w2β2 nM	DR6w19 nM	DR5w11 nM	DR8w2 nM	DR147 Degen	Broad Degen (5/8)
39.0217	RWCIPWQRLLTASL	2340	CEA.10	8.2	542	357	--	--	318	--	--	3	5
39.0219	EVLLLVHNLPQHLEG	2341	CEA.50	2.0	52	53	40	--	1.0	588	408	3	7
39.0220	GREIIYPPNASLIQNL	2342	CEA.97	8.1	484	45	24	8333	2.9	6897	5904	3	5
39.0221	EIYYPNAASLIQNL	2343	CEA.99	14	1154	156	57	--	11	--	--	2	4
39.0223	DTGFYFTLHVIKSDLV	2344	CEA.116	69	1731	227	506	800	3889	2500	790	2	5
39.0226	YLWWVVNNQSLPVSPR	2345	CEA.176	0.60	8.0	42	110	2105	2.3	29	1065	3	6
39.0228	QYSWFVNQTFQQSTQ	2346	CEA.268	192	80	926	--	6061	5833	370	--	3	4
39.0233	RTTVKTTIVSAELPK	2347	CEA.488	455	7031	317	364	--	700	--	--	2	4
39.0239	NNSTIVKSTIVSASGT	2348	CEA.665	91	25	676	3138	--	51	--	4083	3	4
39.0240	NSIVKSTIVSASGT	2349	CEA.666	78	25	329	3957	--	76	--	2882	3	4

-- indicates binding affinity = 10,000nM.



Table XXXI. DR3 binding

Peptide	Sequence	SEQ ID NO:	Source	DR3 nM
39.0313	QNIIQNDTGFYTLHV	2350	CEA.110	938
39.0314	LHVIKSDLVNEEATG	2351	CEA.122	2308
39.0315	KSDLVNEEATGQFRV	2352	CEA.126	--
39.0316	SDLVNEEATGQFRVY	2353	CEA.127	--
39.0317	NEEATGQFRVYPELP	2354	CEA.131	--
39.0318	QFRVYPELPKPSISS	2355	CEA.137	--
39.0319	AVAFTCPEPETQDATY	2356	CEA.162	--
39.0320	TASYKCETQNPVSAR	2357	CEA.210	--
39.0321	NVLYGPDAVTISPLN	2358	CEA.232	--
39.0322	ISPLNTSYRSGENLN	2359	CEA.242	--
39.0323	SGSYTCQAHNSDTGL	2360	CEA.294	--
39.0324	TITVYAEPPKKPFTS	2361	CEA.315	--
39.0325	SNPVEDEDAVALTCE	2362	CEA.332	--
39.0326	AVALTCEPEIQNTTY	2363	CEA.340	--
39.0327	NQSLPVSPRLQLSND	2364	CEA.360	--
39.0328	RLQLSNDNRNLTLSS	2365	CEA.368	938
39.0329	ECGIQNELSVDHSDP	2366	CEA.392	--
39.0330	QNELSVDHSDPVILN	2367	CEA.396	3659
39.0331	NVLYGPDDPTISPSY	2368	CEA.410	--
39.0332	GVNLSSLSCCHAASNPP	2369	CEA.430	--
39.0333	TITVSAELPKPSISS	2370	CEA.493	--
39.0334	AVAFTCPEAQNTTY	2371	CEA.518	--
39.0335	SDPVTLVDVLYGPDT	2372	CEA.582	--
39.0336	DVLYGPDTPIISPPD	2373	CEA.588	--
39.0337	GANLNLSCHSASNPS	2374	CEA.608	--

-- indicates binding affinity =10,000nM.



Table XXXII. HTLC Candidate Epitopes

Peptide	Sequence	SEQ ID NO:	Motif	Source	DR1 nM	DR4w4 nM	DR7 nM	DR3 nM	DR2w2 β1 nM	DR2w2 β2 nM	DR5w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR147 Cross-reactivity	Broad Cross-reactivity	DR3 Binder
39.0217	RWCIPWQRLLTASL	1 2375	DR sup	CEA.10	8.2	542	357	--	827	--	318	--	--	3	5	0
39.0219	EVLILLYVHNLPQHFLFG	1 2376	DR sup	CEA.50	2.0	52	53	336	40	--	1.0	588	408	3	7	1
39.0220	GREIYPNNAEJJQJN	1 2377	DR sup	CEA.97	8.1	484	45	1123	24	8333	2.9	6897	5904	3	5	0
39.0313	QNIQNDTGFTTLHV	1 2378	DR3	CEA.110	1136	>8182	--	938	867	--	9.7	--	--	0	2	1
39.0223	DTCGFYTLHVIRKSDLV	1 2379	DR sup	CEA.116	69	1731	227	--	506	800	3889	2500	790	2	5	0
39.0226	YLWWVNNQSPLPVSPR	1 2380	DR sup	CEA.176	0.60	8.0	42	2310	110	2105	2.3	29	1065	3	6	0
39.0328	RQLQSNNDNRKTLTLLS	1 2381	DR3	CEA.368	--	>8182	--	938	--	--	729	--	--	0	1	1

-- indicates binding affinity = 10,000nM

all done